=> index bioscience medicine

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F3 337 CAPLUS
F4 291 BIOSIS
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F34 1 CROPU
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FILE 'CAPLUS' ENTERED AT 16:09:07 ON 11 JUL 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE 'BIOSIS' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'SCISEARCH' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'CABA' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'ESBIOBASE' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'MEDLINE' ENTERED AT 16:09:07 ON 11 JUL 2006

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FILE 'AGRICOLA' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'PASCAL' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'BIOTECHNO' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'LIFESCI' ENTERED AT 16:09:07 ON 11 JUL 2006

FILE 'IFIPAT' ENTERED AT 16:09:07 ON 11 JUL 2006

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=> s L1
L2 2113 L1

=> S (alpha or beta)(s) L2
L3 732 (ALPHA OR BETA)(S) L2

=> s plant (s)L3
L4 232 PLANT (S) L3

=> s (rice or oryzae or sativa)(s) L4
L5 27 (RICE OR ORYZAE OR SATIVA)(S) L4

=> dup rem L5
PROCESSING COMPLETED FOR L5
L6 25 DUP REM L5 (2 DUPLICATES REMOVED)

=> (motif or domain) (s) L6
(MOTIF IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> S (motif or domain) (s) L6

L7 2 (MOTIF OR DOMAIN) (S) L6

=> d ibib abs L6 1-25

L6 ANSWER 1 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2006:132792 USPATFULL <<LOGINID::20060711>>
TITLE: Rice promoters
INVENTOR(S): Hatzfeld, Yves, Lille, FRANCE
Broekaert, Willem, Dilbeek, BELGIUM

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2006112442	A1	20060525
APPLICATION INFO.:	US 2004-525647	A1	20040204 (10)
	WO 2004-EP50081		20040204
			20050224 PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	EP 2003-75331	20030204

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Barbara E Johnson, 436 Seventh Avenue, 700 Koppers Building, Pittsburgh, PA, 15219-1818, US
NUMBER OF CLAIMS: 32
EXEMPLARY CLAIM: 1-18
NUMBER OF DRAWINGS: 11 Drawing Page(s)
LINE COUNT: 2897
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides several promoters isolated from Oryza sativa, which promoters are capable of driving and/or regulating the expression of an operably linked nucleic acid in a plant. The expression patterns of the promoters according to the invention have been studied in Oryza sativa and some of the promoters displayed specific activity in particular cells, tissues or organs of the plant, while others displayed constitutive expression throughout substantially the whole plant. Some promoters showed weak expression, while others were strongly active.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 2 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2006:23249 USPATFULL <<LOGINID::20060711>>
TITLE: Identification of novel e2f target genes and use thereof
INVENTOR(S): Inze, Dirk, Moorsel-Aalst, BELGIUM

Veylder, Lieven, Drongen, BELGIUM
Vlieghe, Kobe, Aalter, BELGIUM

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2006021088	A1	20060126
APPLICATION INFO.:	US 2003-531475	A1	20031020 (10)
	WO 2003-EP11658		20031020
			20050415 PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	EP 2002-79408	20021018

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: NIXON & VANDERHYE, PC, 901 NORTH GLEBE ROAD, 11TH FLOOR, ARLINGTON, VA, 22203, US
NUMBER OF CLAIMS: 39
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 10 Drawing Page(s)
LINE COUNT: 6959
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention concerns a method for altering characteristics of a plant. The invention describes the identification of genes that are upregulated or downregulated in transgenic plants overexpressing E2Fa/DPa and the use of such sequences to alter plant characteristics. A preferred way for altering characteristics of a plant comprises modifying expression of one or more nucleic acid sequences and or modifying level and/or activity of one or more proteins, which nucleic acids and/or proteins are essentially similar to any one or more of SEQ ID NO 1 to 2755. Some of the genes identified in the present invention have an E2Fa target consensus sequence in their 5' upstream region. The identified genes play a role in a variety of biological processes, such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism, transcription factors etc.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 3 OF 25 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2006-173803 [18] WPIDS
DOC. NO. NON-CPI: N2006-149939
DOC. NO. CPI: C2006-058240
TITLE: Improving plant growth characteristics e.g. increased yield, comprises increasing the activity of an RNA-binding protein in a plant and selecting plants having improved growth characteristics.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): FRANKARD, V; REUZEAU, C; SANZ MOLINERO, A I
PATENT ASSIGNEE(S): (CROP-N) CROPDESIGN NV
COUNTRY COUNT: 111
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2006018432	A2	20060223	(200618)*	EN	78

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IS IT KE LS LT LU LV MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KM KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NG NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SM SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2006018432	A2	WO 2005-EP54034	20050816

PRIORITY APPLN. INFO: US 2004-602680P 20040819; EP 2004-103926 20040816

AN 2006-173803 [18] WPIDS

AB WO2006018432 A UPAB: 20060315

NOVELTY - Improving (M1) plant growth characteristics, comprises increasing activity in a plant of an RNA-binding protein or its homolog and optionally selecting plants having improved growth characteristics.

DETAILED DESCRIPTION - Improving (M1) plant growth characteristics, comprises:

(a) increasing activity in a plant of an RNA-binding protein or its homolog (P1), where (P1) is either a polypeptide (P2) having RNA-binding activity and comprising either 2 or 3 RNA recognition motifs (RRMs) and a motif having at least 75% sequence identity to motif I and/or motif having at least 50% sequence identity to motif II, or an RBP1 polypeptide or its homolog (P3) having RNA-binding activity, two RRM domains, motif (III) or (IV), allowing for up to three amino acid substitutions and any conservative change in the motifs, and having, in increasing order of preference, at least 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% sequence identity to At1g58470 protein sequence having a fully defined 360 amino acid (SEQ ID No: 15) sequence, given in the specification, and optionally selecting plants having improved growth characteristics; or

(b) introducing and expressing in a plant a nucleic acid (N1) or its functional variant encoding (P1).

Pro-Tyr-Glu-Ala-Ala-Val-Val-Ala-Leu-Pro-Val-Val-Val-Lys-Glu-Arg-Leu-Val-Arg-Ile-Leu-Arg-Leu-Gly-Ile-Ala-Thr-Arg-Tyr-Asp (motif I)

Arg-Phe-Asp-Pro-Phe-Thr-Gly-Glu-Pro-Tyr-Lys-Phe-Asp-Pro (motif II)

Lys-Ile-Phe-Val-Gly-Gly-Leu (motif III)

Arg-Pro-Arg-Gly-Phe-Gly-Phe (Motif IV)

(b) introducing and expressing in a plant a nucleic acid (N1) or its functional variant encoding (P1). INDEPENDENT CLAIMS are also included for the following:

(1) plants (I) obtainable by (M1);

(2) a construct (C1) comprising a RNA-binding protein encoding nucleic acid or its variant (N2) that encodes (P2), one or more control sequence capable of driving expression of the nucleic acid sequence, and optionally a transcription termination sequence;

(3) a construct (C2) comprising an rbp1-encoding nucleic acid or its variant (N3), which encodes (P3), one or more control sequence capable of driving expression of the nucleic acid sequence, and optionally a transcription termination sequence;

(4) plants (II) transformed with (C1) or (C2);

(5) producing (M2) a transgenic plant having improved growth characteristics, comprising introducing (N2) or (N3) into a plant, and cultivating the plant cell under conditions promoting plant growth and development;

(6) a transgenic plant (III) having improved growth characteristics resulting from an RNA-binding protein-encoding nucleic acid or its variant introduced into the plant;

(7) a transgenic (IV) plant having improved growth characteristics resulting from an rbp1 nucleic acid or its variant introduced into the plant;

(8) harvestable parts of any one of (I)-(IV);

(9) use of (N2), (N3), (P3) or (P4) in modifying the growth characteristics of plants, in particular in improving yield, especially seed yield; and

(10) use of (P3) or (P4) as a molecular marker.

USE - (M1) Is useful for improving plant growth characteristics, where the improved plant growth characteristic is chosen from increased yield relative to corresponding wild-type plants, increased plant biomass, increased growth rate, increased seed yield, increased seed biomass, increased number of (filled) seeds, increased seed size, increased seed volume, increased harvest index, and increased thousand kernal weight (TKW). (M2) Is useful for producing a transgenic plant having improved growth characteristics. (N2), (N3), (P3) Or (P4) is useful for modifying the growth characteristics of plants, in particular in improving yield, especially seed yield. (P3) Or (P4) is useful as a molecular marker (all claimed).

Dwg.0/40

L6 ANSWER 4 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:888009 CAPLUS <<LOGINID::20060711>>
DOCUMENT NUMBER: 143:243059
TITLE: DNA sequences of rice shoot vascular bundle specific promoters and their use for regulation of plant growth
INVENTOR(S): Ichikawa, Hiroaki; Tanaka, Yuji; Nakamura, Hidemitsu; Sasaki, Takaharu; Kikuchi, Hisashi
PATENT ASSIGNEE(S): National Institute of Agrobiological Resources NIAR, Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 18 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2005224112	A2	20050825	JP 2004-33362	20040210

PRIORITY APPLN. INFO.: JP 2004-33362 20040210
AB This invention provides DNA sequences of five rice shoot vascular bundle specific promoters. The promoters were identified from gene encoding rice proline rich protein, PRP1, .beta.-expansin and three unknown proteins. The promoters regulated gene expression in rice shoot vascular bundle which can be used for regulation of the uptake of nutrition into plants.

L6 ANSWER 5 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2006:60865 CAPLUS <<LOGINID::20060711>>
DOCUMENT NUMBER: 144:165331
TITLE: cDNA library for rice pollination related gene and its application
INVENTOR(S): Lan, Lefu; Xue, Yongbiao; Chen, Wei; Lai, Ying; Kong, Zhaosheng; Zhang, Yansheng; Han, Bin
PATENT ASSIGNEE(S): Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 120 pp.
CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 1618964	A	20050525	CN 2003-10115043	20031120

PRIORITY APPLN. INFO.: CN 2003-10115043 20031120
AB The invention provides DNA sequences for rice pollination related gene sequence homolog with the same function. The invention relates to expression vectors and cell lines contg. any gene from cDNA library. The invention also relates to application of the above cDNA library for research of mol. mechanism in pollination process and rice breeding.

L6 ANSWER 6 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2005:307709 USPATFULL <<LOGINID::20060711>>
TITLE: Plants having improved growth characteristics and a method for making the same
INVENTOR(S): Frankard, Valerie, Bruxelles, BELGIUM
Reuzeau, Christophe, Tocane, FRANCE
PATENT ASSIGNEE(S): CropDesign N.V. (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005268358	A1	20051201
APPLICATION INFO.:	US 2005-60029	A1	20050217 (11)

	NUMBER	DATE
PRIORITY INFORMATION:	EP 2004-102392	20040528
	US 2004-576250P	20040602 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: THE WEBB LAW FIRM, P.C., 700 KOPPERS BUILDING, 436 SEVENTH AVENUE, PITTSBURGH, PA, 15219, US
NUMBER OF CLAIMS: 34
EXEMPLARY CLAIM: 1-24
NUMBER OF DRAWINGS: 16 Drawing Page(s)
LINE COUNT: 2245
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention concerns a method for improving plant growth by increasing activity of DP protein in shoot tissue. The invention also relates to transgenic plants having improved growth characteristics, which plants have increased expression of a DP nucleic acid specifically in shoot-tissue. The increased expression of the nucleic acid encoding a DP protein, according to the methods of the present invention, may be mediated by a shoot-tissue-specific promoter.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 7 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2005:282833 USPATFULL <<LOGINID::20060711>>
TITLE: Root-specific expansin gene regulating root growth and obstacle-touching stress resistance in the plant
INVENTOR(S): Lee, Jong Seob, Seoul, KOREA, REPUBLIC OF
Lee, Dong-Keun, Seoul, KOREA, REPUBLIC OF
Ahn, Ji Hoon, Seoul, KOREA, REPUBLIC OF
Song, Sang-Kee, Seoul, KOREA, REPUBLIC OF
Choi, Yang Do, Seoul, KOREA, REPUBLIC OF
PATENT ASSIGNEE(S): SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005246795	A1	20051103
APPLICATION INFO.:	US 2003-660499	A1	20030912 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	KR 2003-19069	20030327

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: JHK Law, P.O. Box 1078, La Canada, CA, 91012-1078, US
NUMBER OF CLAIMS: 16
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 15 Drawing Page(s)
LINE COUNT: 1085
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to root-specific expansin gene to regulating root growth and obstacle-touching stress resistance in the plant, and more particularly to a root growth regulating gene, GmEXP1, isolated from soybean (Glycine max), an expansin polypeptide encoded by the gene and a method for enhancing root growth of plants by overexpression of the gene in the plants.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 8 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2005:268141 USPATFULL <<LOGINID::20060711>>
TITLE: Novel expansin polynucleotides, related polypeptides and methods of use
INVENTOR(S): Cosgrove, Daniel J., Pennsylvania Furnace, PA, UNITED STATES
Wu, Yajun, Logan, UT, UNITED STATES
PATENT ASSIGNEE(S): The Penn State Research Foundation, University Park, PA, UNITED STATES (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2005233458	A1	20051020
APPLICATION INFO.:	US 2005-142525	A1	20050601 (11)

RELATED APPLN. INFO.: Division of Ser. No. US 2002-125001, filed on 18 Apr 2002, PENDING

	NUMBER	DATE

PRIORITY INFORMATION: US 2001-285050P 20010419 (60)
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MCKEE, VOORHEES & SEASE, P.L.C., ATTN: PENNSYLVANIA STATE UNIVERSITY, 801 GRAND AVENUE, SUITE 3200, DES MOINES, IA, 50309-2721, US
NUMBER OF CLAIMS: 3
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 3 Drawing Page(s)
LINE COUNT: 2516
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to beta expansin polypeptides, nucleotide sequences encoding the same and regulatory elements and their use in altering cell wall structure in plants. Nucleic acid constructs comprising a beta expansin sequence operably linked to a promoter, or other regulatory sequence are disclosed as well as vectors, plant cells, plants, and transformed seeds containing such constructs are provided. Methods for the use of such constructs in repressing or inducing expression of a beta expansin sequences in a plant are also provided as well as methods for harvesting transgenic expansin proteins. In addition, methods are provided for inhibiting or improving cell wall structure in plants by repression or induction of expansin sequences in plants.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 9 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2005:177208 USPATFULL <<LOGINID::20060711>>
TITLE: Methods for identifying gibberellin responsive genes using cultured vegetable cells
INVENTOR(S): Minami, Eiichi, Ibaraki, JAPAN
Shibuya, Naoto, Kanagawa, JAPAN
Day, Robert B., Berkeley, CA, UNITED STATES

	NUMBER	KIND	DATE

PATENT INFORMATION: US 2005153288 A1 20050714
APPLICATION INFO.: US 2003-496530 A1 20021220 (10)
WO 2002-JP13376 20021220

	NUMBER	DATE

PRIORITY INFORMATION: JP 2001-388993 20011221
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SALIWANCHIK LLOYD & SALIWANCHIK, A PROFESSIONAL ASSOCIATION, PO BOX 142950, GAINESVILLE, FL, 32614-2950, US
NUMBER OF CLAIMS: 6
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Page(s)
LINE COUNT: 1285
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB To date, those skilled in the art have never considered that cultured plant cells respond to gibberellins. However, to comprehensively and conveniently identify and isolate gibberellin responsive genes, cultured cells, which are uniform and easy to handle, are appropriate. Considering the advantages of cultured cells, the present inventors developed methods for identifying and isolating gibberellin responsive genes using cultured cells. After pre-culturing cells in an auxin-free medium, they examined whether or not changes in gene expression could be detected. As a result, it was surprisingly revealed that changes in the expression of some genes could be detected after gibberellin treatment.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 10 OF 25 IFIPAT COPYRIGHT 2006 IFI on STN
AN 10984690 IFIPAT;IFIUDB;IFICDB <<LOGINID::20060711>>
TITLE: METHOD FOR MODIFYING PLANT MORPHOLOGY, BIOCHEMISTRY AND PHYSIOLOGY
INVENTOR(S): Frankard; Valerie, Brussel, BE
Schmulling; Thomas, Berlin, DE
Werner; Tomas, Berlin, DE
PATENT ASSIGNEE(S): Unassigned
AGENT: DILWORTH & BARRESE, LLP, 333 EARLE OVINGTON BLVD., UNIONDALE, NY, 11553, US

	NUMBER	PK	DATE
PATENT INFORMATION:	US 2005223429	A1	20051006
APPLICATION INFORMATION:	US 2005-57473		20050214

	APPLN. NUMBER	DATE	GRANTED PATENT NO. OR STATUS
CONTINUATION-IN-PART OF:	WO 2001-EP6833	20010618	
CONTINUATION-IN-PART OF:	US 2001-14101	20011210	PENDING
CONTINUATION-IN-PART OF:	US 2004-871304	20040618	PENDING

	NUMBER	DATE
PRIORITY APPLN. INFO.:	US 2004-544393P	20040213 (Provisional)
FAMILY INFORMATION:	US 2005223429	20051006

DOCUMENT TYPE: Utility
Patent Application - First Publication
FILE SEGMENT: CHEMICAL
APPLICATION

PARENT CASE DATA:

This application claims the benefit of U.S. Provisional Application Ser. No. 60/544,393, filed Feb. 13, 2004 and is a continuation in part of U.S. Ser. No. 10/871,304, filed Jun. 18, 2004, which is a continuation-in-part application of U.S. Ser. No. 10/014,101, filed Dec. 10, 2001, which is a continuation-inpart of PCT/EP01/06833, having an international filing date of Jun. 18, 2001.

NUMBER OF CLAIMS: 28 22 Figure(s).
DESCRIPTION OF FIGURES:
FIG. 1. Schematic representation of ***plant*** cytokinin oxidase genes.
FIG. 2. Alignment of ***plant*** cytokinin oxidase amino acid sequences.
FIG. 3. Northern blot analysis of AtCKX1-expressing tobacco and Arabidopsis plants.
FIG. 4: Growth characteristics of 35S::AtCKX1 transgenic Arabidopsis plants.
FIG. 5: Phenotype of AtCKX2 overexpressing Arabidopsis plants.
FIG. 6. Northern blot analysis of AtCKX2-expressing tobacco and Arabidopsis plants.
FIG. 7. Shoot phenotype of AtCKX1 and AtCKX2 expressing tobacco plants.
FIG. 8. Root phenotype of AtCKX expressing transgenic tobacco plants.
FIG. 9: Growth of axillary shoot meristems in 35S::AtCKX1 expressing tobacco plants.
FIG. 10: Histology of shoot meristems, leaves and root meristems of AtCKX1 overexpressing tobacco plants versus wild type (WT) tobacco.
FIG. 11: Northern blot analysis of AtCKX3 and AtCKX4-expressing tobacco plants.
FIG. 12: Reciprocal grafts of AtCKX2 transgenic tobacco plants and wild type plants.
FIG. 13: Phenotype of Arabidopsis seeds, embryos and seedlings.
FIG. 14: Seed weight of wild type and two independent clones for each of the four investigated AtCKX genes. Average weight obtained by analysing five different batches of 200 seeds for each clone.
FIG. 15: Schematic presentation of the entry clone p41, containing CDS0427 2 within the AttL1 and AttL2 sites for Gateway (reg) cloning in the pDONR201 backbone. CDS0427 2 is the internal code for the Arabidopsis thaliana CKX2 coding sequence (SEQ ID NO: 44). This vector contains also a bacterial kanamycine-resistance cassette and a bacterial origin of replication.
FIG. 16: Binary vector p37 for the expression in Oryza ***sativa*** of the

Arabidopsis thaliana CKX2 gene under the control of the PRO0218 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0218-CDS0427 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX2 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 17: Binary vector p35 for the expression in Oryza ***sativa*** of the Arabidopsis thaliana CKX2 gene under the control of the PRO0090 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0090-CDS0427 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX2 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 18: Schematic presentation of the entry clone p049, containing CDS1499 2 within the AttL1 and AttL2 sites for Gateway (reg) cloning in the pDONR201 backbone. CDS1499 2 is the internal code for the Arabidopsis thaliana CKX1 coding sequence (SEQ ID NO:48). This vector contains also a bacterial kanamycine-resistance cassette and a bacterial origin of replication.

FIG. 19: Binary vector p051 for the expression in Oryza ***sativa*** of the Arabidopsis thaliana CKX1 gene under the control of the PRO0218 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0218-CDS1499 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX1 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 20: Schematic presentation of the expression vector p39 for the expression in plants of Arabidopsis CKX under the control of the PRO0109 promoter (SEQ ID NO 56). CDS0427 2 is the internal code for CKX cDNA as presented in SEQ ID NO 50. To be expressible in the ***plant*** , the CKX expression cassette with the PRO0109 promoter and the double terminator sequence (Ter3 and Ter4), is located within the left border (LB repeat) and the right border (RB repeat) of the Ti plasmid. Within these Tborders, also a screenable marker and a selectable marker are cloned, each under a constitutive promoter (Prom1 and 2) and followed by a terminator sequence (Ter1 and 2). This vector furthermore contains an origin of replication (pBR322 (ori+bom)) for bacterial replication and a selectable marker (Sm/SpR) for bacterial selection.

FIG. 21: Phenotype of ***rice*** plants transformed with SEQ ID NO 50 under control of the promoter as represented in SEQ ID NO 56. The plants on the left are nullizygous control plants.

FIGS. 22A-C show the expression pattern of the ***beta*** ***expansine*** EXPB9 promoter (SEQ ID NO: 60). GUS staining is visible in young flowers of A plants (A) and in other young expanding tissues of B plants (B) and C plants (C).

AB The present invention relates to methods for stimulating root growth and/or enhancing the formation of lateral or adventitious roots and/or altering root geotropism comprising expression of a cytokinin oxidase or comprising expression of another protein that reduces the level of active cytokinins in plants or plant parts. Also provided by the present invention are methods for increasing seed size and/or weight, embryo size and/or weight, and cotyledon size and/or weight. The methods comprise expression of a cytokinin oxidase or expression of another protein that reduces the level of active cytokinins in plants or plant parts. Methods and compositions for increasing seed yield are also provided. The invention also relates to isolated plant cytokinin oxidase proteins, nucleic acid sequences encoding cytokinin oxidase proteins as well as to vectors, host cells, transgenic cells and plants comprising such sequences. The use of these sequences for improving rootrelated characteristics including increasing yield and/or enhancing early vigor

and/or modifying root/shoot ratio and/or improving resistance to lodging and/or increasing drought tolerance and/or promoting in vitro propagation of explants and/ or modifying cell fate and/or plant development and/or plant morphology and/or plant biochemistry and/or plant physiology, is also provided. The invention also relates to methods for identifying and obtaining proteins and compounds interacting with cytokinin oxidase proteins as well as the use of such proteins and/or compounds as plant growth regulators or herbicides.

CLMN 28 22 Figure(s).

FIG. 1. Schematic representation of ***plant*** cytokinin oxidase genes.

FIG. 2. Alignment of ***plant*** cytokinin oxidase amino acid sequences.

FIG. 3. Northern blot analysis of AtCKX1-expressing tobacco and Arabidopsis plants.

FIG. 4: Growth characteristics of 35S::AtCKX1 transgenic Arabidopsis plants.

FIG. 5: Phenotype of AtCKX2 overexpressing Arabidopsis plants.

FIG. 6. Northern blot analysis of AtCKX2-expressing tobacco and Arabidopsis plants.

FIG. 7. Shoot phenotype of AtCKX1 and AtCKX2 expressing tobacco plants.

FIG. 8. Root phenotype of AtCKX expressing transgenic tobacco plants.

FIG. 9: Growth of axillary shoot meristems in 35S::AtCKX1 expressing tobacco plants.

FIG. 10: Histology of shoot meristems, leaves and root meristems of AtCKX1 overexpressing tobacco plants versus wild type (WT) tobacco.

FIG. 11: Northern blot analysis of AtCKX3 and AtCKX4-expressing tobacco plants.

FIG. 12: Reciprocal grafts of AtCKX2 transgenic tobacco plants and wild type plants.

FIG. 13: Phenotype of Arabidopsis seeds, embryos and seedlings.

FIG. 14: Seed weight of wild type and two independent clones for each of the four investigated AtCKX genes. Average weight obtained by analysing five different batches of 200 seeds for each clone.

FIG. 15: Schematic presentation of the entry clone p41, containing CDS0427 2 within the AttL1 and AttL2 sites for Gateway (reg) cloning in the pDONR201 backbone. CDS0427 2 is the internal code for the Arabidopsis thaliana CKX2 coding sequence (SEQ ID NO: 44). This vector contains also a bacterial kanamycine-resistance cassette and a bacterial origin of replication.

FIG. 16: Binary vector p37 for the expression in Oryza ***sativa*** of the Arabidopsis thaliana CKX2 gene under the control of the PRO0218 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0218-CDS0427 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX2 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 17: Binary vector p35 for the expression in Oryza ***sativa*** of the Arabidopsis thaliana CKX2 gene under the control of the PRO0090 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0090-CDS0427 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX2 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 18: Schematic presentation of the entry clone p049, containing CDS1499 2 within the AttL1 and AttL2 sites for Gateway (reg) cloning in the pDONR201 backbone. CDS1499 2 is the internal code for the Arabidopsis thaliana CKX1 coding sequence (SEQ ID NO:48). This vector contains also a bacterial kanamycine-resistance cassette and a bacterial origin of replication.

FIG. 19: Binary vector p051 for the expression in Oryza ***sativa*** of the Arabidopsis thaliana CKX1 gene under the control of the PRO0218 promoter. This vector contains a T-DNA derived from the Ti plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)). From the left border to the right border, this T-DNA contains: a selectable and a screenable marker for selection of transformed plants, each under control of a constitutive promoter; the PRO0218-CDS1499 2zein and rbcS-deltaGA double terminator cassette for expression of the Arabidopsis thaliana CKX1 gene. This vector also contains an origin of replication from pBR322 for bacterial replication and a selectable marker (Spe/SmeR) for bacterial selection with spectinomycin and streptomycin.

FIG. 20: Schematic presentation of the expression vector p39 for the expression in plants of Arabidopsis CKX under the control of the PRO0109 promoter (SEQ ID NO 56). CDS0427 2 is the internal code for CKX cDNA as presented in SEQ ID NO 50. To be expressible in the ***plant*** , the CKX expression cassette with the PRO0109 promoter and the double terminator sequence (Ter3 and Ter4), is located within the left border (LB repeat) and the right border (RB repeat) of the Ti plasmid. Within these Tborders, also a screenable marker and a selectable marker are cloned, each under a constitutive promoter (Prom1 and 2) and followed by a terminator sequence (Ter1 and 2). This vector furthermore contains an origin of replication (pBR322 (ori+bom)) for bacterial replication and a selectable marker (Sm/SpR) for bacterial selection.

FIG. 21: Phenotype of ***rice*** plants transformed with SEQ ID NO 50 under control of the promoter as represented in SEQ ID NO 56. The plants on the left are nullizygous control plants.

FIGS. 22A-C show the expression pattern of the ***beta*** ***expansine*** EXPB9 promoter (SEQ ID NO: 60). GUS staining is visible in young flowers of A plants (A) and in other young expanding tissues of B plants (B) and C plants (C).

L6 ANSWER 11 OF 25 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-630728 [64] WPIDS
DOC. NO. CPI: C2005-189263
TITLE: New construct comprising a cyclin D3-encoding nucleic acid preferentially expressed in the shoots, is useful in improving plant and seed yields, such as increased seed biomass.
DERWENT CLASS: C06 D16
INVENTOR(S): FRANKARD, V
PATENT ASSIGNEE(S): (CROP-N) CROPDESIGN NV
COUNTRY COUNT: 109
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2005085452	A1	20050915	(200564)*	EN	51

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IS IT KE LS LT LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SM SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2005085452	A1	WO 2005-EP51033	20050308

PRIORITY APPLN. INFO: US 2004-553418P 20040316; EP 2004-100991 20040310
AN 2005-630728 [64] WPIDS
AB WO2005085452 A UPAB: 20051006
NOVELTY - New construct comprising a cyclin D3-encoding nucleic acid or its functional variant, or its functional variant, a promoter capable of

preferentially expressing the nucleic acid in shoots, particularly in the cell expansion zone of vegetative shoots, and optionally a transcription termination sequence.

DETAILED DESCRIPTION - New construct (I) comprising a cyclin D3-encoding nucleic acid or its functional variant, preferably a cyclin D3-encoding nucleic acid of SEQ ID NO: 1 or its functional variant, encoding a cyclin D3 polypeptide of SEQ ID NO: 2 or its functional variant; a promoter capable of preferentially expressing the nucleic acid in shoots, particularly in the cell expansion zone of vegetative shoots; and optionally a transcription termination sequence;

INDEPENDENT CLAIMS are also included for the following:

(1) a method for the production of a transgenic plant having improved yield relative to corresponding wild type plants, comprising introducing into a plant or plant cell a cyclin 03-encoding nucleic acid or its variant, preferably a cyclin D3-encoding nucleic acid with 1086 bp (SEQ ID NO: 1) or its functional variant, which nucleic acid or its functional variant encodes a cyclin D3 polypeptide or its functional variant, which polypeptide has a fully defined sequence of 361 amino acids (SEQ ID NO: 2) or its functional variant and which nucleic acid is operably linked to a promoter capable of expressing the nucleic acid in shoots, particularly in the cell expansion zone of vegetative shoots, and cultivating the plant cell to promote regeneration and mature plant growth;

(2) plants obtained by any of the methods mentioned;

(4) a plant transformed with (I) and having improved yield relative to corresponding wild type plants, comprising a nucleic acid encoding a cyclin D3 or its functional variant under the control of a promoter capable of expressing the nucleic acid in shoots; and

(5) harvestable parts of a transgenic plant of (2) or (4).

ACTIVITY - Plant Growth Regulant.

MECHANISM OF ACTION - Gene Therapy.

USE - (I) useful in improving yield, in particular in increasing seed yield that includes increased seed biomass, increased number of (filled) seeds, increased seed size, increased seed volume, increased harvest index and increased thousand kernel weight.

Dwg.0/6

L6 ANSWER 12 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 2005:1269206 CAPLUS <<LOGINID::20060711>>

DOCUMENT NUMBER: 144:325613

TITLE: Characterization and transcriptional expression of the .alpha.-expansin gene family in rice

AUTHOR(S): Shin, Jun-Hye; Jeong, Dong-Hoon; Park, Min Chul; An, Gynheung

CORPORATE SOURCE: National Research Laboratory of Plant Functional Genomics, Pohang University of Science and Technology Biotech Center, Division of Molecular and Life Sciences, Pohang University of Science and Technology, Pohang, 790-784, S. Korea

SOURCE: Molecules and Cells (2005), 20(2), 210-218
CODEN: MOCEEK; ISSN: 1016-8478

PUBLISHER: Korean Society for Molecular and Cellular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The rice genome contains at least 28 EXPA (.alpha.-expansin) genes. We have obtained near full-length cDNAs from the previously uncharacterized genes. Anal. of these newly identified clones together with the 12 identified earlier showed that the EXPA genes contain up to two introns and encode proteins of 240 to 291 amino acid residues. The EXPA proteins contain three conserved motifs: eight cysteine residues at the N-terminus, four tryptophan residues at the C-terminus, and a histidine-phenylalanine-aspartate motif in the central region. EXPA proteins could be divided into six groups based on their sequence similarity. Most were strongly induced in two-day-old seedlings and in the roots of one-week-old plants. However, only 14 genes were expressed in the aboveground organs, and their patterns were quite diverse. Transcript levels of EXPA7, 14, 15, 18, 21, and 29 were greater in stems, while EXPA2, 4, 5, 6, and 16 were highly expressed in both stem and sheath but not in leaf blade. EXPA1 is leaf blade-preferential, and EXP9 is leaf sheath-preferential. Most of the root-expressed genes were more strongly expressed in the dividing zone. However, the Group 2 EXPA genes were also strongly expressed in both

mature and dividing zones, while EXPA9 was preferentially expressed in the elongation zone. Fourteen EXPA genes were expressed in developing panicles, with some being expressed during most developmental stages, others only as the panicles matured. These diverse expression patterns of EXPA genes suggest that in general they have distinct roles in plant growth and development.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 25 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2005:554970 BIOSIS <<LOGINID::20060711>>

DOCUMENT NUMBER: PREV200510335377

TITLE: Genetic and epigenetic control of plant growth and development. Genes of auxin biosynthesis and auxin-regulated genes controlling plant cell division and extension.

AUTHOR(S): Tsygankova, V. A.; Galkina, L. A.; Musatenko, L. I.; Sytnik, K. M.

SOURCE: Biopolimery i Kletka, (MAR-APR 2005) Vol. 21, No. 2, pp. 107-133.
CODEN: BIKLEK. ISSN: 0233-7657.

DOCUMENT TYPE: Article
General Review; (Literature Review)

LANGUAGE: Ukrainian

ENTRY DATE: Entered STN: 7 Dec 2005
Last Updated on STN: 7 Dec 2005

AB In the review a spectrum of enzymes' genes determining different ways of indole-3-acetic acid (IAA) biosynthesis identified at Arabidopsis is given: the TRP1 gene of antranilat phosphoribosyltransferase 1, TRP3 gene of tryptophane synthase and family NIT genes of nitrilase, catalysing tryptophane-independent way of IAA biosynthesis from precursor indole-3-acetonitrile; CYP79B and CYP83B1 genes (members of family cytochromes P450 genes), controlling IAA biosynthesis from tryptophane; the enzymes' genes, catalysing of the IAA biosynthesis from indole-3-butyric acid: the PXA1 and PEX14 genes of peroxisomal membrane proteins - the ABC-ATPas family members, the PEX5 and PEX7 genes of cytoplasmic protein receptors, genes of peroxisomal matrix proteins-enzymes (acx3 gene of acyl-CoA oxidase, aim1 gene of multifunctional protein and ped1 gene of thiolase); enzymes' genes catalysing synthesis of IAA-conjugates and their hydrolysis - the genes of IAGLc synthase, IAInos transferase, serin carboxypeptidase-like IAInos acyltransferase and IAR3 gene of IAA-Ala hydrolase. The nomenclature and classification of the auxin-regulated genes responsible for the cell division are presented: cyclin genes and activated by them cyclin-dependent protein kinases, as well as genes of numerous family of mitogen-activated protein kinases. The auxin-induced genes of enzymes participating in biosynthesis and hydrolysis of polysaccharides components of ***plant*** cell walls in the period of their growth by extension are considered in detail: the EI gene of endo-1,3:1,4- ***beta*** -D-glucanase and EXOII gene of exo- ***beta*** -D-glucanase, numerous families XET genes of xyloglucan endotransglycosylases, ZeEXP genes of ***expansins*** , AtFUT genes of xyloglucan-specific ***beta*** -1,6- and ***beta*** -1,2-fucosyltransferases and glycosyltransferases, CSL genes of xyloglucan glucan synthases and ***beta*** -1,4-mannan synthases, MUR genes xyloglucan galactosyltransferases as well as AtXT1 gene and homologous AtGT2-7 genes xyloglucan xylosyltransferases at Arabidopsis; the XS1 gene of xylansynthase at ***rice*** , and also GS1 gene of glucansynthase at corn. A possible role of cell wall protein - extensin (encoded by the auxin-regulated HRGP gene) in the plants defence from pathogens and unfavourable factors of external environment is discussed.

L6 ANSWER 14 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:678402 CAPLUS <<LOGINID::20060711>>

DOCUMENT NUMBER: 141:203533

TITLE: Sequences of rice promoters and their uses in regulating expression of heterologous nucleic acid and promoting plant growth in transgenic plant

INVENTOR(S): Hatzfeld, Yves; Broekaert, Willem

PATENT ASSIGNEE(S): Cropdesign N.V., Belg.
SOURCE: PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004070039	A2	20040819	WO 2004-EP50081	20040204
WO 2004070039	A3	20050324		
AU 2004209624	A1	20040819	AU 2004-209624	20040204
EP 1532257	A2	20050525	EP 2004-707946	20040204
CN 1748032	A	20060315	CN 2004-80003528	20040204
US 2006112442	A1	20060525	US 2005-525647	20050224

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI

RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK

PRIORITY APPLN. INFO.: EP 2003-75331 A 20030204
WO 2004-EP50081 W 20040204

AB The present invention provides the DNA sequence of 22 promoters isolated from Oryza sativa, which promoters are capable of driving and/or regulating the expression of a operably linked nucleic acid in a plant. The expression patterns of the promoters according to the present invention have been studied in Oryza sativa and some of the promoters displayed specific activity in particular cells, tissues or organs of the plant, while others displayed constitutive expression throughout substantially the whole plant. Some promoters showed weak expression, while others were strongly active. The promoters are isolated from RCc3, .beta.-amylase, cellulose synthase, proteinase inhibitor Rgpi9, expansine EXPB9, structural protein, caffeoyl-CoA 3-O-methyltransferase, prolamine RP5, methionine aminopeptidase, uclacyanin 3-like protein, 26S proteasome regulatory particle non-ATPase subunit 11, 40S ribosomal protein, chlorophyll a/b-binding protein precursor, protochlorophyllide reductase, chitinase Cht-3, WS118, aquaporine, High mobility group protein, reversibly glycosylated protein RGP1, cytosolic MDH, RAB21, and Cdc2-1 genes.

L6 ANSWER 15 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2004:172453 USPATFULL <<LOGINID::20060711>>
TITLE: Beta-expansins as cell wall loosening agents, compositions thereof and methods of use
INVENTOR(S): Cosgrove, Daniel J., Pennsylvania Furnace, PA, UNITED STATES
PATENT ASSIGNEE(S): The Penn State Research Foundation, Universal Park, PA, UNITED STATES, 16802-7000 (non-U.S. corporation)

NUMBER	KIND	DATE
PATENT INFORMATION: US 2004132617	A1	20040708
APPLICATION INFO.: US 2003-730866	A1	20031209 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-71252, filed on 1 May 1998, GRANTED, Pat. No. US 6682738

NUMBER	DATE
PRIORITY INFORMATION: US 1997-45445P	19970502 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MCKEE, VOORHEES & SEASE, P.L.C., ATTN: PENNSYLVANIA STATE UNIVERSITY, 801 GRAND AVENUE, SUITE 3200, DES MOINES, IA, 50309-2721

NUMBER OF CLAIMS: 40
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 9 Drawing Page(s)
LINE COUNT: 1955
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to proteins belonging to a novel class of proteins designated as .beta.-expansins, a composition comprising such proteins, isolated polynucleotides encoding .beta.-expansins, methods for using the polynucleotides and proteins of the invention and methods for identifying, isolating and purifying expansins, including a and .beta.-expansins. Beta-expansins of the invention have the property of altering physical properties of a plant cell wall, such as for example by loosening or expanding plant cell walls.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 16 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2004:144526 USPATFULL <<LOGINID::20060711>>
TITLE: Plant cell wall loosening activity of group 2/3 allergens of grass pollen
INVENTOR(S): Li, Lian-Chao, State College, PA, UNITED STATES
Cosgrove, Daniel J., Pennsylvania Furnace, PA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004110190	A1	20040610
APPLICATION INFO.:	US 2003-628296	A1	20030728 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-399688P	20020729 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MCKEE, VOORHEES & SEASE, P.L.C., ATTN: PENNSYLVANIA STATE UNIVERSITY, 801 GRAND AVENUE, SUITE 3200, DES MOINES, IA, 50309-2721
NUMBER OF CLAIMS: 29
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 1846
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides nucleic acids and polypeptide sequences for a novel class of expansin-related proteins, designated group 2/3 allergen, which comprise the group 2 and group 3 allergens from grass, a purified group 3 allergen Lol p 3, and method of using the nucleic acids sequences and proteins of the invention. Group 2/3 allergens of the invention are significant wall-loosening agents. They are capable of altering cell wall properties, which may effect growth, flexibility, and mechanical strength in tissues in which they are expressed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 17 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2004:21476 USPATFULL <<LOGINID::20060711>>
TITLE: .beta.-expansins as cell wall loosening agents, compositions thereof and methods of use
INVENTOR(S): Cosgrove, Daniel J., Pennsylvania Furnace, PA, United States
PATENT ASSIGNEE(S): The Penn State Research Foundation, University Park, PA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6682738	B1	20040127
APPLICATION INFO.:	US 1998-71252		19980501 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-45445P	19970502 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Nolan, Patrick J.
LEGAL REPRESENTATIVE: McKee, Voorhees & Sease, P.L.C.
NUMBER OF CLAIMS: 11
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Figure(s); 9 Drawing Page(s)
LINE COUNT: 1804
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to proteins belonging to a novel class of proteins designated as .beta.-expansins, a composition comprising such proteins, isolated polynucleotides encoding .beta.-expansins, methods for using the polynucleotides and proteins of the invention and methods for identifying, isolating and purifying expansins, including .alpha. and .beta.-expansins. Beta-expansins of the invention have the property of altering physical properties of a plant cell wall, such as for example by loosening or expanding plant cell walls.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 18 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2003:239346 USPATFULL <<LOGINID::20060711>>
TITLE: Expansin protein and polynucleotides and methods of use
INVENTOR(S): Multani, Dilbag S., Urbandale, IA, UNITED STATES
Johal, Gurmukh S., Urbandale, IA, UNITED STATES
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003167506	A1	20030904
APPLICATION INFO.:	US 2002-102349	A1	20020320 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-324182P	20010921 (60)
	US 2001-277847P	20010322 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PIONEER HI-BRED INTERNATIONAL INC., 7100 N.W. 62ND AVENUE, P.O. BOX 1000, JOHNSTON, IA, 50131
NUMBER OF CLAIMS: 28
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 2290
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions for modulating plant growth, strength and flexibility are provided. Nucleotide sequences encoding maize expansin proteins are provided. The sequence can be used in expression cassettes for modulating growth, stalk strength and flexibility. Transformed plants, plant cells, tissues, and seed are also provided. Methods for rapidly identifying and isolating a Mu-tagged recessive gene mutation in a F1 generation plant, and identification and isolation of its associated wild-type gene are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 19 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2003:196076 USPATFULL <<LOGINID::20060711>>
TITLE: Genes that are modulated by posttranscriptional gene silencing
INVENTOR(S): Zhu, Tong, San Diego, CA, UNITED STATES
Wang, Xun, San Diego, CA, UNITED STATES
Chang, Hur-Song, San Diego, CA, UNITED STATES
Briggs, Steven P., Del Mar, CA, UNITED STATES
Cooper, Bret, La Jolla, CA, UNITED STATES
Glazebrook, Jane, San Diego, CA, UNITED STATES
Goff, Stephen A., Encinitas, CA, UNITED STATES
Katagiri, Fumiaki, San Diego, CA, UNITED STATES
Kreps, Joel, Carlsbad, CA, UNITED STATES
Moughamer, Todd, San Diego, CA, UNITED STATES

Provart, Nicholas, Toronto, CANADA
Ricke, Darrell, San Diego, CA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003135888	A1	20030717
APPLICATION INFO.:	US 2002-259165	A1	20020926 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-368327P	20020327 (60)
	US 2001-325277P	20010926 (60)
	US 2002-370620P	20020404 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: TORREY MESA RESEARCH INSTITUTE, INTELLECTUAL PROPERTY DEPARTMENT, 3115 MERRYFIELD ROW, SAN DIEGO, CA, 92121
NUMBER OF CLAIMS: 67
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 7516
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method to identify genes that are modulated by posttranscriptional gene silencing as well as regulatory elements and methods to modulate gene expression by posttranscriptional gene silencing.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 20 OF 25 USPATFULL on STN
ACCESSION NUMBER: 2003:78613 USPATFULL <<LOGINID::20060711>>
TITLE: Novel expansin polynucleotides, related polypeptides and methods of use
INVENTOR(S): Cosgrove, Daniel J., Pennsylvania Furnace, PA, UNITED STATES
Wu, Yajun, Logan, UT, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003054533	A1	20030320
	US 7001743	B2	20060221
APPLICATION INFO.:	US 2002-125001	A1	20020418 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-285050P	20010419 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: MCKEE, VOORHEES & SEASE, P.L.C., ATTN: PENNSYLVANIA STATE UNIVERSITY, 801 GRAND AVENUE, SUITE 3200, DES MOINES, IA, 50309-2721
NUMBER OF CLAIMS: 21
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 3 Drawing Page(s)
LINE COUNT: 2167
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to beta expansin polypeptides, nucleotide sequences encoding the same and regulatory elements and their use in altering cell wall structure in plants. Nucleic acid constructs comprising a beta expansin sequence operably linked to a promoter, or other regulatory sequence are disclosed as well as vectors, plant cells, plants, and transformed seeds containing such constructs are provided. Methods for the use of such constructs in repressing or inducing expression of a beta expansin sequences in a plant are also provided as well as methods for harvesting transgenic expansin proteins. In addition, methods are provided for inhibiting or improving cell wall structure in plants by repression or induction of expansin sequences in plants.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 21 OF 25 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-093115 [08] WPIDS
DOC. NO. CPI: C2003-023361
TITLE: Expansin polynucleotides, useful for inhibiting or improving cell wall structure in plants.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): COSGROVE, D J; WU, Y
PATENT ASSIGNEE(S): (COSG-I) COSGROVE D J; (WUYY-I) WU Y; (PENN-N) PENN STATE RES FOUND
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002086066	A2	20021031	(200308)*	EN	74
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
US 2003054533	A1	20030320	(200323)		
AU 2002256276	A1	20021105	(200433)		
US 2005233458	A1	20051020	(200569)		
AU 2002256276	A8	20051013	(200611)		
US 7001743	B2	20060221	(200615)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002086066	A2	WO 2002-US12263	20020418
US 2003054533	A1 Provisional	US 2001-285050P	20010419
		US 2002-125001	20020418
AU 2002256276	A1	AU 2002-256276	20020418
US 2005233458	A1 Provisional	US 2001-285050P	20010419
	Div ex	US 2002-125001	20020418
		US 2005-142525	20050601
AU 2002256276	A8	AU 2002-256276	20020418
US 7001743	B2 Provisional	US 2001-285050P	20010419
		US 2002-125001	20020418

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002256276	A1 Based on	WO 2002086066
AU 2002256276	A8 Based on	WO 2002086066

PRIORITY APPLN. INFO: US 2002-125001 20020418; US 2001-285050P 20010419; US 2005-142525 20050601
AN 2003-093115 [08] WPIDS
AB WO 200286066 A UPAB: 20030204
NOVELTY - An isolated polynucleotide comprising:
(a) a sequence comprising 1273 bp encoding B2 or B4 beta expansin polypeptide comprising 282 or 308 amino acids;
(b) a sequence that selectively hybridizes to or having at least 50% identity with (a);
(c) a complement of (a) or (b); or
(d) a sequence comprising at least 25 contiguous nucleotides of (a)-(c), is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a recombinant expression cassette comprising the polynucleotide;
(2) a vector comprising the recombinant expression cassette;
(3) a host cell comprising the recombinant expression cassette;
(4) a transformed plant comprising the polynucleotide;
(5) a plant seed comprising the polynucleotide;

(6) altering cell wall characteristics in a plant; or
(7) making a beta expansin.
USE - The polynucleotide is useful for inhibiting or improving cell wall structure in plants by repression or induction of expansin sequences in plants.
Dwg.0/5

L6 ANSWER 22 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:887522 CAPLUS <<LOGINID::20060711>>
DOCUMENT NUMBER: 138:133843
TITLE: Expression of .alpha.-expansin and expansin-like genes in deepwater rice
AUTHOR(S): Lee, Yi; Kende, Hans
CORPORATE SOURCE: Department of Energy Plant Research Laboratory, Michigan State University, East Lansing, MI, 48824-1312, USA
SOURCE: Plant Physiology (2002), 130(3), 1396-1405
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Biologists
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Previously, we have studied the expression and regulation of four .alpha.- and 14 .beta.-expansin genes in deepwater rice (Oryza sativa). We now report on the structure, expression, and regulation of 22 addnl. .alpha.-expansin (Os-EXP) genes, four expansin-like (Os-EXPL) genes, and one expansin-related (Os-EXPR) gene, which have recently been identified in the expressed sequence tag and genomic databases of rice. .alpha.-Expansins are characterized by a series of conserved Cys residues in the N-terminal half of the protein, a histidine-phenylalanine-aspartate (HFD) motif in the central region, and a series of tryptophan residues near the carboxyl terminus. Of the 22 addnl. .alpha.-expansin genes, five are expressed in internodes and leaves, three in coleoptiles, and nine in roots, with high transcript levels in the growing regions of these organs. Transcripts of five .alpha.-expansin genes were found in roots only. Expression of five .alpha.-expansin genes was induced in the internode by treatment with gibberellin (GA) and by wounding. The wound response resulted from excising stem sections or from piercing pinholes into the stem of intact plants. EXPL proteins lack the HFD motif and have two addnl. Cys residues in their C- and N-terminal regions. The positions of conserved tryptophan residues at the C-terminal region are different from those of .alpha.- and .beta.-expansins. Expression of the Os-EXPL3 gene is correlated with elongation and slightly induced by applied GA. However, the expression of the Os-EXPL1 and Os-EXPL2 genes showed limited correlation with cell elongation and was not induced by GA. We found no expression of the Os-EXPR1 gene in the organs examd.
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 23 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:775693 CAPLUS <<LOGINID::20060711>>
DOCUMENT NUMBER: 136:34771
TITLE: Expression of .beta.-expansins is correlated with internodal elongation in deepwater rice
AUTHOR(S): Lee, Yi; Kende, Hans
CORPORATE SOURCE: Department of Energy Plant Research Laboratory, Michigan State University, East Lansing, MI, 48824-1312, USA
SOURCE: Plant Physiology (2001), 127(2), 645-654
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Biologists
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Fourteen putative rice (Oryza sativa) .beta.-expansin genes, Os-EXPB1 through Os-EXPB14, were identified in the expressed sequence tag and genomic databases. The DNA and deduced amino acid sequences are highly conserved in all 14 .beta.-expansins. They have a series of conserved C (cysteine) residues in the N-terminal half of the protein, an HFD (histidine-phenylalanine-aspartate) motif in the central region, and a series of W (tryptophan) residues near the carboxyl terminus. Five .beta.-expansin genes are expressed in deepwater rice internodes, with

esp. high transcript levels in the growing region. Expression of four .beta.-expansin genes in the internode was induced by treatment with gibberellin and by wounding. The wound response resulted from excising stem sections or from piercing pinholes into the stem of intact plants. The level of wound-induced .beta.-expansin transcripts declined rapidly 5 h after cutting of stem sections. We conclude that the expression of .beta.-expansin genes is correlated with rapid elongation of deepwater rice internodes, it is induced by gibberellin and wounding, and wound-induced .beta.-expansin mRNA appears to turn over rapidly.
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 24 OF 25 Elsevier BIOBASE COPYRIGHT 2006 Elsevier Science B.V. on STN DUPLICATE
ACCESSION NUMBER: 2001245431 ESBIOBASE <<LOGINID::20060711>>
TITLE: Expansins: Ever-expanding numbers and functions
AUTHOR: Lee Y.; Choi D.; Kende H.
CORPORATE SOURCE: Y. Lee, MSU-DOE Plant Research Laboratory, Michigan State University, East Lansing, MI 48824, United States.
E-mail: hkende@msu.edu
SOURCE: Current Opinion in Plant Biology, (2001), 4/6 (527-532), 41 reference(s)
CODEN: COPBFZ ISSN: 1369-5266
DOCUMENT TYPE: Journal; General Review
COUNTRY: United Kingdom
LANGUAGE: English
SUMMARY LANGUAGE: English
AB ***Expansins*** were first identified as cell-wall-loosening proteins that, at least in part, mediate pH-dependent extension of the ***plant*** cell wall and growth of the cell. More recently, it has been realized that ***expansins*** belong to two protein families, the . ***alpha*** .- and . ***beta*** .- ***expansins*** , and that they appear to be involved in regulating, besides cell expansion, a variety of ***plant*** processes, including morphogenesis, softening of fruits, and growth of the pollen tube of grasses through the stigma and the style. The Arabidopsis genome contains 26 . ***alpha*** .- ***expansin*** genes and the ***rice*** genome at least 26. There are more . ***beta*** .- ***expansin*** genes in monocots than in dicots, at least 14 in ***rice*** and five in Arabidopsis. ***Expansin*** genes are differentially regulated by environmental and hormonal signals, and hormonal regulatory elements have been found in their promoter regions. An analysis of exon/intron structure led to the hypothesis that . ***alpha*** .- and . ***beta*** .- ***expansins*** evolved from a common ancestral gene.

L6 ANSWER 25 OF 25 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:629130 CAPLUS <<LOGINID::20060711>>
DOCUMENT NUMBER: 133:319565
TITLE: Expression of .alpha.-expansin genes in young seedlings of rice (Oryza sativa L.)
AUTHOR(S): Huang, Jirong; Takano, Tetsuo; Akita, Shigemi
CORPORATE SOURCE: Graduate School of Agricultural and Life Sciences, Department of Agricultural and Environmental Biology, University of Tokyo, Tokyo, 113-8657, Japan
SOURCE: Planta (2000), 211(4), 467-473
CODEN: PLANAB; ISSN: 0032-0935
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Rice is the only cereal in which germination and coleoptile elongation occur in hypoxia or anoxia. Little is known of the mol. basis directly underlying coleoptile cell extension. In this paper, we describe the expression of .alpha.-expansin genes in embryos during seed development and young seedlings grown under various oxygen concns. The genes Os-EXP2 and Os-EXP1 were predominantly expressed in the developing seeds, mainly in newly developed leaves, coleoptiles, and seminal roots. These expansins expressed in the developing seeds may give cells the potential to expand after seed imbibition begins. In coleoptiles, Os-EXP4 and Os-EXP2 mRNAs were greatly induced by submergence, while they were weakly

detected in aerobic or anoxic conditions. Under submerged soil conditions, the signals hybridized with probes Os-EXP4 and Os-EXP2 in coleoptiles were strongest when coleoptiles elongated in the water layer. These data show that expansin gene expression is highly correlated with coleoptile elongation in response to oxygen concns. The Os-EXP4 gene was also expressed in leaves, mesocotyls, and coleorhizas of young seedlings. The growth of these tissues was also correlated with the presence of expansins. Therefore, the evidence derived from this study clearly demonstrates that expansins are indispensable for the growing tissues of rice seedlings.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L7 ANSWER 1 OF 2 USPATFULL on STN
ACCESSION NUMBER: 2003:239346 USPATFULL <<LOGINID::20060711>>
TITLE: Expansin protein and polynucleotides and methods of use
INVENTOR(S): Multani, Dilbag S., Urbandale, IA, UNITED STATES
Johal, Gurmukh S., Urbandale, IA, UNITED STATES
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003167506	A1	20030904
APPLICATION INFO.:	US 2002-102349	A1	20020320 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-324182P	20010921 (60)
	US 2001-277847P	20010322 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: PIONEER HI-BRED INTERNATIONAL INC., 7100 N.W. 62ND AVENUE, P.O. BOX 1000, JOHNSTON, IA, 50131
NUMBER OF CLAIMS: 28
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 2290
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions for modulating plant growth, strength and flexibility are provided. Nucleotide sequences encoding maize expansin proteins are provided. The sequence can be used in expression cassettes for modulating growth, stalk strength and flexibility. Transformed plants, plant cells, tissues, and seed are also provided. Methods for rapidly identifying and isolating a Mu-tagged recessive gene mutation in a F1 generation plant, and identification and isolation of its associated wild-type gene are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 2 OF 2 USPATFULL on STN
ACCESSION NUMBER: 2003:196076 USPATFULL <<LOGINID::20060711>>
TITLE: Genes that are modulated by posttranscriptional gene silencing
INVENTOR(S): Zhu, Tong, San Diego, CA, UNITED STATES
Wang, Xun, San Diego, CA, UNITED STATES
Chang, Hur-Song, San Diego, CA, UNITED STATES
Briggs, Steven P., Del Mar, CA, UNITED STATES
Cooper, Bret, La Jolla, CA, UNITED STATES
Glazebrook, Jane, San Diego, CA, UNITED STATES
Goff, Stephen A., Encinitas, CA, UNITED STATES
Katagiri, Fumiaki, San Diego, CA, UNITED STATES
Kreps, Joel, Carlsbad, CA, UNITED STATES
Moughamer, Todd, San Diego, CA, UNITED STATES
Provart, Nicholas, Toronto, CANADA
Ricke, Darrell, San Diego, CA, UNITED STATES

	NUMBER	KIND	DATE

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PATENT INFORMATION: US 2003135888 A1 20030717
APPLICATION INFO.: US 2002-259165 A1 20020926 (10)

NUMBER DATE
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PRIORITY INFORMATION: US 2002-368327P 20020327 (60)
US 2001-325277P 20010926 (60)
US 2002-370620P 20020404 (60)
DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: TORREY MESA RESEARCH INSTITUTE, INTELLECTUAL PROPERTY DEPARTMENT, 3115 MERRYFIELD ROW, SAN DIEGO, CA, 92121
NUMBER OF CLAIMS: 67
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Page(s)
LINE COUNT: 7516
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method to identify genes that are modulated by posttranscriptional gene silencing as well as regulatory elements and methods to modulate gene expression by posttranscriptional gene silencing.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L1 QUE EXPANSIN#

L2 2113 S L1
L3 732 S (ALPHA OR BETA)(S) L2
L4 232 S PLANT (S)L3
L5 27 S (RICE OR ORYZAE OR SATIVA)(S) L4
L6 25 DUP REM L5 (2 DUPLICATES REMOVED)
L7 2 S (MOTIF OR DOMAIN) (S) L6

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